

SEQUENCE LISTING

SEQ ID NO: 1

SEQUENCE LENGTH: 1877

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE

ORGANISM: mouse

SEQUENCE DESCRIPTION:

CCATCCTAAT ACGACTCACT ATA 23

GGGCTCGAGC GGCCGCCCGG GCAGGTGCAG GTAGCAGTGA CCCTCTGA 71

GGCGTTTGGTGCTCCGGTAACCACCACGGCTGTAGAGCGAGTGTTGCC 119

ATGGAACCGATCAGTGTGAGTATATACACTTCTGATAACTACTCTGAA 167

MetGluProIleSerValSerIleTyrThrSerAspAsnTyrSerGlu

1 5 10 15

GAAGTGGGGTCTGGAGACTATGACTCCAACAAGGAACCCTGCTTCCGG 215

GluValGlySerGlyAspTyrAspSerAsnLysGluProCysPheArg

20 25 30

GATGAAAACGTCCATTTCAATAGGATCTTCCTGCCCACCATCTACTTC 263

AspGluAsnValHisPheAsnArgIlePheLeuProThrIleTyrPhe

35 40 45

ATCATCTTCTTGACTGGCATAGTCGGCAATGGATTGGTGATCCTGGTC 311

IleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuVal

50 55 60

ATGGGTTACCAGAAGAAGCTAAGGAGCATGACGGACAAGTACCGGCTG 359

MetGlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeu

65 70 75 80

CACCTGTCAGTGGCTGACCTCCTCTTTGTCATCACACTCCCCTTCTGG 407

HisLeuSerValAlaAspLeuLeuPheValIleThrLeuProPheTrp

85 90 95

GCAGTTGATGCCATGGCTGACTGGTACTTTGGGAAATTTTGTGTAAG 455

AlaValAspAlaMetAlaAspTrpTyrPheGlyLysPheLeuCysLys

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100 105 110  
GCTGTCCATATCATCTACACTGTCAACCTCTACAGCAGCGTTCTCATC 503  
AlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeuIle  
115 120 125  
CTGGCCTTCATCAGCCTGGACCGGTACCTCGCCATTGTCCACGCCACC 551  
LeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThr  
130 135 140  
AACAGTCAAAGGCCAAGGAAACTGCTGGCTGAAAAGGCAGTCTATGTG 599  
AsnSerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrVal  
145 150 155 160  
GGCGTCTGGATCCCAGCCCTCCTCCTGACTATACCTGACTTCATCTTT 647  
GlyValTrpIleProAlaLeuLeuLeuThrIleProAspPheIlePhe  
165 170 175  
GCCGACGTCAGCCAGGGGGACATCAGTCAGGGGGATGACAGGTACATC 697  
AlaAspValSerGlnGlyAspIleSerGlnGlyAspAspArgTyrIle  
180 185 190  
TGTGACCGCCTTTACCCCGATAGCCTGTGGATGGTGGTGTTCATTC 743  
CysAspArgLeuTyrProAspSerLeuTrpMetValValPheGlnPhe  
195 200 205  
CAGCATATAATGGTGGGTCTCATCCTGCCCGGCATCGTCATCCTCTCC 791  
GlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSer  
210 215 220  
TGTTACTGCATCATCATCTCTAAGCTGTCACACTCCAAGGGCCACCAG 839  
CysTyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGln  
225 230 235 240  
AAGCGCAAGGCCCTCAAGACGACAGTCATCCTCATCCTAGCTTTCTTT 887  
LysArgLysAlaLeuLysThrThrValIleLeuIleLeuAlaPhePhe  
245 250 255  
GCCTGCTGGCTGCCATATTATGTGGGGATCAGCATCGACTCCTTCATC 935  
AlaCysTrpLeuProTyrTyrValGlyIleSerIleAspSerPheIle  
260 265 270  
CTTTTGGGAGTCATCAAGCAAGGATGTGACTTCGAGAGCATTGTGCAC 983  
LeuLeuGlyValIleLysGlnGlyCysAspPheGluSerIleValHis  
275 280 285

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AAGTGGATCTCCATCACAGAGGCCCTCGCCTTCTTCCACTGTTGCCTG 1031  
LysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeu  
290 295 300  
AACCCCATCCTCTATGCCTTCCTCGGGGCCAAGTTCAAAAGCTCTGCC 1079  
AsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAla  
305 310 315 320  
CAGCATGCACTCAACTCCATGAGCAGAGGCTCCAGCCTCAAGATCCTT 1127  
GlnHisAlaLeuAsnSerMetSerArgGlySerSerLeuLysIleLeu  
325 330 335  
TCCAAAGGAAAGCGGGGTGGACACTCTTCCGTCTCCACGGAGTCAGAA 1175  
SerLysGlyLysArgGlyGlyHisSerSerValSerThrGluSerGlu  
340 345 350  
TCCTCCAGTTTTTCACTCCAGCTAACCCCTTATGCAAAGACTTATATAAT 1223  
SerSerSerPheHisSerSer  
355 359  
ATATATATATATATGATAAAGAACTTTTTTATGTTACACATTTTCCAG 1271  
ATATAAGAGACTGACCAGTCTTGACAGTTTTTTTTTTTTTTAATTG 1319  
ACTGTTGGGAGTTTATGTTCCCTCTAGTTTTTGTGAGGTTTGAATTAAT 1367  
TTATATAAATATTGTTTTTTGTTTGTTCATGTGAATGAGCGTCTAGG 1415  
CAGGACCTGTGGCCAAGTTCTTAGTAGCTGTTTATCTGTGTGTAGGAC 1463  
TGTAAGAACTGTAGAGGAAGAACTGAACATTCCAGAATGTGTGGTAAA 1511  
TTGAATAAAGCTAGCCGTGATCCTCAGCTGTTGCTGCATAATCTCTTC 1559  
ATTCCGAGGAGCACCCACCCACCCACCCACCCACCCATTCTTAA 1607  
ATTGTTTGGTTATGCTGTGTGATGGTTTGGTTTTTTTTTTGTTGT 1655  
TGTTGTTGTTTTTTTTTCTGTAAAAGATGGCACTTAAAACCAAAGCC 1703  
TGAAATGGTGGTAGAAATGCTGGGGTTTTTTTTTGTGTTGTTGTTTTT 1751  
CAGTTTTCAAGAGTAGATTGACTTCAGTCCCTACAAATGTACAGTCTT 1799  
GTATTACATTGTTAATAAAAGTCAATGATAAACTTAAAAAAAAAAAAA 1847  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1877

SEQ ID NO: 2

SEQUENCE LENGTH: 690

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

09367052.080699

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE

ORGANISM: mouse

SEQUENCE DESCRIPTION:

CTG

3

Leu

1

CACCTGTCAGTGGCTGACCTCCTCTTTGTCATCACACTCCCCTTCTGG 51

HisLeuSerValAlaAspLeuLeuPheValIleThrLeuProPheTrp

5

10

15

GCAGTTGATGCCATGGCTGACTGGTACTTTGGGAAATTTTGTGTAAG 99

AlaValAspAlaMetAlaAspTrpTyrPheGlyLysPheLeuCysLys

20

25

30

GCTGTCCATATCATCTACACTGTCAACCTCTACAGCAGCGTTCTCATC 147

AlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeuIle

35

40

45

CTGGCCTTCATCAGCCTGGACCGGTACCTCGGAAATTGTCCACGCCACC 195

LeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThr

50

55

60

65

AACAGTCAAAGGCCAAGGAAACTGCTGGCTGAAAAGGCAGTCTATGTG 243

AsnSerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrVal

70

75

80

GGCGTCTGGATCCCAGCCCTCCTCCTGACTATACCTGACTTCATCTTT 291

GlyValTrpIleProAlaLeuLeuLeuThrIleProAspPheIlePhe

85

90

95

GCCGACGTCAGCCAGGGGGACATCAGTCAGGGGGATGACAGGTACATC 339

AlaAspValSerGlnGlyAspIleSerGlnGlyAspAspArgTyrIle

100

105

110

TGTGACCGCCTTTACCCCGATAGCCTGTGGATGGTGGTGTTCATTC 387

CysAspArgLeuTyrProAspSerLeuTrpMetValValPheGlnPhe

115

120

125

CAGCATATAATGGTGGGTCTCATCCTGCCCGGCATCGTCATCCTCTCC 435

GlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSer

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130 135 140 145  
 TGTTACTGCATCATCATCTCTAAGCTGTCACACTCCAAGGGCCACCAG 483  
 CysTyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGln  
 150 155 160  
 AAGCGCAAGGCCCTCAAGACGACAGTCATCCTCATCCTAGCTTTCTTT 531  
 LysArgLysAlaLeuLysThrThrValIleLeuIleLeuAlaPhePhe  
 165 170 175  
 GCCTGCTGGCTGCCATATTATGTGGGGATCAGCATCGACTCCTTCATC 579  
 AlaCysTrpLeuProTyrTyrValGlyIleSerIleAspSerPheIle  
 180 185 190  
 CTTTTGGGAGTCATCAAGCAAGGATGTGACTTCGAGAGCATTTGTGCAC 627  
 LeuLeuGlyValIleLysGlnGlyCysAspPheGluSerIleValHis  
 195 200 205  
 AAGTGGATCTCCATCACAGAGGCCCTCGCCTTCTTCCACTGTTGCCTG 675  
 LysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeu  
 210 215 220 225  
 AACCCCATCCTCTAT 690  
 AsnProIleLeuTyr  
 230

SEQ ID NO: 3  
 SEQUENCE LENGTH: 685  
 SEQUENCE TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 ORIGINAL SOURCE

ORGANISM: mouse  
 SEQUENCE DESCRIPTION:  
 CCATCCTAATACGACTCACTATA 23  
 GGGCTCGAGCGGCCCGCCGGGCAGGTGCAGGTAGCAGTGACCCTCTGA 71  
 GGCGTTTGGTGCTCCGGTAACCACCACGGCTGTAGAGCGAGTGTTGCC 119  
 ATGGAACCGATCAGTGTGAGTATATACACTTCTGATAACTACTCTGAA 167  
 MetGluProIleSerValSerIleTyrThrSerAspAsnTyrSerGlu

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1 5 10 15  
GAAGTGGGGTCTGGAGACTATGACTCCACAAGGAACCCTGCTTCCGG 215  
GluValGlySerGlyAspTyrAspSerAsnLysGluProCysPheArg  
20 25 30  
GATGAAAACGTCCATTTCAATAGGATCTTGCTGCCCACCATCTACTTC 263  
AspGluAsnValHisPheAsnArgIlePheLeuProThrIleTyrPhe  
35 40 45  
ATCATCTTCTTGACTGGCATAGTCGGCAATGGATTGGTGATCCTGGTC 311  
IleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuVal  
50 55 60  
ATGGGTTACCAGAAGAAGCTAAGGAGCATGACGGACAAGTACCGGCTG 359  
MetGlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeu  
65 70 75 80  
CACCTGTCAGTGGCTGACCTCCTCTTTGTGCATCACACTCCCCTTCTGG 407  
HisLeuSerValAlaAspLeuLeuPheValIleThrLeuProPheTrp  
85 90 95  
GCAGTTGATGCCATGGCTGACTGGTACTTTGGGAATTTTGTGTAAG 455  
AlaValAspAlaMetAlaAspTrpTyrPheGlyLysPheLeuCysLys  
100 105 110  
GCTGTCCATATCATCTACACTGTCAACCTCTACAGCAGCGTTCTCATC 503  
AlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeuIle  
115 120 125  
CTGGCCTTCATCAGCCTGGACCGGTACCTCGCCATTGTCCACGCCACC 551  
LeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThr  
130 135 140  
AACAGTCAAAGGCCAAGGAACTGCTGGCTGAAAAGGCAGTCTATGTG 599  
AsnSerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrVal  
145 150 155 160  
GGCGTCTGGATCCCAGCCCTCCTCCTGACTATACCTGACTTCATCTTT 647  
GlyValTrpIleProAlaLeuLeuLeuThrIleProAspPheIlePhe  
165 170 175  
GCCGACGTCAGCCAGGGGACATCAGTCAGGGGGATGA 685  
AlaAspValSerGlnGlyAspIleSerGlnGlyAsp  
180 185

009080"25029660

SEQ ID NO: 4

SEQUENCE LENGTH: 1694

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

ORIGINAL SOURCE

ORGANISM: mouse

SEQUENCE DESCRIPTION:

ATATACACTTCTGATAACTACTCTGAA 27  
IleTyrThrSerAspAsnTyrSerGlu  
1 5  
GAAGTGGGGTCTGGAGACTATGACTCCAACAAGGAACCCTGCTTCCGG 75  
GluValGlySerGlyAspTyrAspSerAsnLysGluProCysPheArg  
10 15 20 25  
GATGAAAACGTCCATTTCAATAGGATCTTCCTGCCCACCATCTACTTC 123  
AspGluAsnValHisPheAsnArgIlePheLeuProThrIleTyrPhe  
30 35 40  
ATCATCTTCTTGACTGGCATAGTCGGCAATGGATTGGTGATCCTGGTC 171  
IleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuVal  
45 50 55  
ATGGGTTACCAGAAGAAGCTAAGGAGCATGACGGACAAGTACCGGCTG 219  
MetGlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeu  
60 65 70  
CACCTGTCAGTGGCTGACCTCCTCTTTGTCATCACACTCCCCTTCTGG 267  
HisLeuSerValAlaAspLeuLeuPheValIleThrLeuProPheTrp  
75 80 85  
GCAGTTGATGCCATGGCTGACTGGTACTTTGGGAAATTTTGTGTAAG 315  
AlaValAspAlaMetAlaAspTrpTyrPheGlyLysPheLeuCysLys  
90 95 100 105  
GCTGTCCATATCATCTACACTGTCAACCTCTACAGCAGCGTTCTCATC 363  
AlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeuIle  
110 115 120  
CTGGCCTTCATCAGCCTGGACCGGTACCTCGCCATTGTGCACGCCACC 411

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LeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThr  
 125 130 135  
 AACAGTCAAAGGCCAAGGAAACTGCTGGCTGAAAAGGCAGTCTATGTG 459  
 AsnSerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrVal  
 140 145 150  
 GGCGTCTGGATCCCAGCCCTCCTGCTGACTATACCTGACTTCATCTTT 507  
 GlyValTrpIleProAlaLeuLeuLeuThrIleProAspPheIlePhe  
 155 160 165  
 GCCGACGTCAGCCAGGGGGACATCAGTCAGGGGGATGACAGGTACATC 555  
 AlaAspValSerGlnGlyAspIleSerGlnGlyAspAspArgTyrIle  
 170 175 180 185  
 TGTGACCGCCTTTACCCCGATAGCCTGTGGATGGTGGTGTTCATTC 603  
 CysAspArgLeuTyrProAspSerLeuTrpMetValValPheGlnPhe  
 190 195 200  
 CAGCATATAATGGTGGGTCTCATCCTGCCCGGCATCGTCATCCTCTCC 651  
 GlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSer  
 205 210 215  
 TGTTACTGCATCATCATCTCTAAGCTGTCACACTCCAAGGGCCACCAG 699  
 CysTyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGln  
 220 225 230  
 AAGCGCAAGGCCCTCAAGACGACAGTCATCCTCATCCTAGCTTTCTTT 747  
 LysArgLysAlaLeuLysThrThrValIleLeuIleLeuAlaPhePhe  
 235 240 245  
 GCCTGCTGGCTGCCATATTATGTGGGGATCAGCATCGACTCCTTCATC 795  
 AlaCysTrpLeuProTyrTyrValGlyIleSerIleAspSerPheIle  
 250 255 260 265  
 CTTTTGGGAGTCATCAAGCAAGGATGTGACTTCGAGAGCATTTGTGCAC 843  
 LeuLeuGlyValIleLysGlnGlyCysAspPheGluSerIleValHis  
 270 275 280  
 AAGTGGATCTCCATCACAGAGGCCCTCGCCTTCTTCCACTGTTGCCTG 891  
 LysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeu  
 285 290 295  
 AACCCCATCCTCTATGCCTTCCTCGGGGCCAAGTTCAAAGCTCTGCC 939  
 AsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAla

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300 305 310  
CAGCATGCACTCAACTCCATGAGCAGAGGCTCCAGCCTCAAGATCCTT 987  
GlnHisAlaLeuAsnSerMetSerArgGlySerSerLeuLysIleLeu  
315 320 325  
TCCAAAGGAAAGCGGGGTGGACACTCTTCCGTCTCCACGGAGTCAGAA 1035  
SerLysGlyLysArgGlyGlyHisSerSerValSerThrGluSerGlu  
330 335 340 345  
TCCTCCAGTTTTTCACTCCAGCTAACCCTTATGCAAAGACTTATATAAT 1083  
SerSerSerPheHisSerSer  
350  
ATATATATATATATGATAAAGAACTTTTTTATGTTACACATTTTCCAG 1131  
ATATAAGAGACTGACCAGTCTTGACAGTTTTTTTTTTTTTTTAATTG 1179  
ACTGTTGGGAGTTTATGTTCCCTCTAGTTTTTGTGAGGTTTGACTIONAAT 1227  
TTATATAAATATTGTTTTTTGTTTGTTCATGTGAATGAGCGTCTAGG 1275  
CAGGACCTGTGGCCAAGTTCTTAGTAGCTGTTTATCTGTGTGTAGGAC 1323  
TGTAAGAACTGTAGAGGAAGAACTGAACATTCCAGAATGTGTGGTAAA 1371  
TTGAATAAAGCTAGCCGTGATCCTCAGCTGTTCTGCATAATCTCTTC 1419  
ATTCCGAGGAGCACCCACCCACCCACCCACCCACCCATTCTTAA 1467  
ATTGTTTGGTTATGCTGTGTGATGGTTTGTGTTGTTTTTTTTTGTGTTGT 1515  
TGTTGTTGTTTTTTTTTTCTGTAAAAGATGGCACTTAAAACCAAAGCC 1563  
TGAAATGGTGGTAGAAATGCTGGGGTTTTTTTTGTTTGTGTTTTTTT 1611  
CAGTTTTCAAGAGTAGATTGACTTCAGTCCCTACAAATGTACAGTCTT 1659  
GTATTACATTGTTAATAAAAAGTCAATGATAAACTT 1694

SEQ ID NO: 5

SEQUENCE LENGTH: 20

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid (synthetic DNA)

FEATURE: 13, 15 (inosine)

SEQUENCE DESCRIPTION:

CTSMGTTTGK CMNTNKCYGA

SEQ ID NO: 6  
SEQUENCE LENGTH: 26  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid (synthetic DNA)  
FEATURE: 8, 9, 17 (inosine)  
SEQUENCE DESCRIPTION:  
TAGAKSANNG GRTTSANRCA RCAGTG 26

SEQ ID NO: 7  
SEQUENCE LENGTH: 25  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid (synthetic DNA)  
SEQUENCE DESCRIPTION:  
TCATCCCCCT GACTGATGTC CCCCT 25

SEQ ID NO: 8  
SEQUENCE LENGTH: 27  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid (synthetic DNA)  
SEQUENCE DESCRIPTION:  
CCATCCTAAT ACGACTCACT ATAGGCC 27

SEQ ID NO: 9  
SEQUENCE LENGTH: 30  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid (synthetic DNA)

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SEQUENCE DESCRIPTION:

CGCGTCGACC ACAACATGCT GTCCACATCA

30

SEQ ID NO: 10

SEQUENCE LENGTH: 30

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:

CGCTCTAGAT TATAAACCAG CCGAGACTTC

30

SEQ ID NO: 11

SEQUENCE LENGTH: 29

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:

CGCGTCGACG TTACCATGGA GGGGATCAG

29

SEQ ID NO: 12

SEQUENCE LENGTH: 32

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:

CGCGCGGCCG CTTAGCTGGA GTGAAACTT GA

32

SEQ ID NO: 13

SEQUENCE LENGTH: 27

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

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TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid (synthetic DNA)  
SEQUENCE DESCRIPTION:  
TAGCGGCCGC GTTGCCATGG AACCGAT 27

SEQ ID NO: 14  
SEQUENCE LENGTH: 27  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid (synthetic DNA)  
SEQUENCE DESCRIPTION:  
GCGTCGACTA AGGGTTAGCT GGAGTGA 27

SEQ ID NO: 15  
SEQUENCE LENGTH: 20  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid (synthetic DNA)  
SEQUENCE DESCRIPTION:  
CTGCACCTGT CAGTGGCTGA 20

SEQ ID NO: 16  
SEQUENCE LENGTH: 27  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid (synthetic DNA)  
SEQUENCE DESCRIPTION:  
TAGATGAGGG GGATTGAGAC AACAGTG 27

SEQ ID NO: 17  
SEQUENCE LENGTH: 359

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SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE

ORGANISM: mouse

SEQUENCE DESCRIPTION:

MetGluProIleSerValSerIleTyrThrSerAspAsnTyrSerGlu

1 5 10 15

GluValGlySerGlyAspTyrAspSerAsnLysGluProCysPheArg

20 25 30

AspGluAsnValHisPheAsnArgIlePheLeuProThrIleTyrPhe

35 40 45

IleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuVal

50 55 60

MetGlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeu

65 70 75 80

HisLeuSerValAlaAspLeuLeuPheValIleThrLeuProPheTrp

85 90 95

AlaValAspAlaMetAlaAspTrpTyrPheGlyLysPheLeuCysLys

100 105 110

AlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeuIle

115 120 125

LeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThr

130 135 140

AsnSerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrVal

145 150 155 160

GlyValTrpIleProAlaLeuLeuLeuThrIleProAspPheIlePhe

165 170 175

AlaAspValSerGlnGlyAspIleSerGlnGlyAspAspArgTyrIle

180 185 190

CysAspArgLeuTyrProAspSerLeuTrpMetValValPheGlnPhe

195 200 205

GlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSer

210 215 220

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CysTyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGln  
225 230 235 240  
LysArgLysAlaLeuLysThrThrValIleLeuIleLeuAlaPhePhe  
245 250 255  
AlaCysTrpLeuProTyrTyrValGlyIleSerIleAspSerPheIle  
260 265 270  
LeuLeuGlyValIleLysGlnGlyCysAspPheGluSerIleValHis  
275 280 285  
LysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeu  
290 295 300  
AsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAla  
305 310 315 320  
GlnHisAlaLeuAsnSerMetSerArgGlySerSerLeuLysIleLeu  
325 330 335  
SerLysGlyLysArgGlyGlyHisSerSerValSerThrGluSerGlu  
340 345 350  
SerSerSerPheHisSerSer  
355 359